

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206-442-6627
- (B) TELEFAX: 206-442-6678
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...1755
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAGAGGCCAA GGGAGGGCTC TGTGCCAGCC CCG ATG AGG ACG CTG CTG ACC ATC	54
Met Arg Thr Leu Leu Thr Ile	
1 5	
TTG ACT GTG GGA TCC CTG GCT GCT CAC GCC CCT GAG GAC CCC TCG GAT	102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp	
10 15 20	
CTG CTC CAG CAC GTG AAA TTC CAG TCC AGC AAC TTT GAA AAC ATC CTG	150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu	
25 30 35	
ACG TGG GAC AGC GGG CCA GAG GGC ACC CCA GAC ACG GTC TAC AGC ATC	198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile	
40 45 50 55	
GAG TAT AAG ACG TAC GGA GAG AGG GAC TGG GTG GCA AAG AAG GGC TGT	246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys	
60 65 70	
CAG CGG ATC ACC CGG AAG TCC TGC AAC CTG ACG GTG GAG ACG GGC AAC	294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn	
75 80 85	

CTC	ACG	GAG	CTC	TAC	TAT	GCC	AGG	GTC	ACC	GCT	GTC	AGT	GCG	GGA	GGC	342
Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	Thr	Ala	Val	Ser	Ala	Gly	Gly	
		90					95					100				
CGG	TCA	GCC	ACC	AAG	ATG	ACT	GAC	AGG	TTC	AGC	TCT	CTG	CAG	CAC	ACT	390
Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	Phe	Ser	Ser	Leu	Gln	His	Thr	
	105					110					115					
ACC	CTC	AAG	CCA	CCT	GAT	GTG	ACC	TGT	ATC	TCC	AAA	GTG	AGA	TCG	ATT	438
Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	Ile	Ser	Lys	Val	Arg	Ser	Ile	
120					125					130					135	
CAG	ATG	ATT	GTT	CAT	CCT	ACC	CCC	ACG	CCA	ATC	CGT	GCA	GGC	GAT	GGC	486
Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	Pro	Ile	Arg	Ala	Gly	Asp	Gly	
				140					145					150		
CAC	CGG	CTA	ACC	CTG	GAA	GAC	ATC	TTC	CAT	GAC	CTG	TTC	TAC	CAC	TTA	534
His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	His	Asp	Leu	Phe	Tyr	His	Leu	
			155					160					165			
GAG	CTC	CAG	GTC	AAC	CGC	ACC	TAC	CAA	ATG	CAC	CTT	GGA	GGG	AAG	CAG	582
Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	Met	His	Leu	Gly	Gly	Lys	Gln	
		170					175					180				
AGA	GAA	TAT	GAG	TTC	TTC	GGC	CTG	ACC	CCT	GAC	ACA	GAG	TTC	CTT	GGC	630
Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	Pro	Asp	Thr	Glu	Phe	Leu	Gly	
	185					190					195					
ACC	ATC	ATG	ATT	TGC	GTT	CCC	ACC	TGG	GCC	AAG	GAG	AGT	GCC	CCC	TAC	678
Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	Ala	Lys	Glu	Ser	Ala	Pro	Tyr	
200					205					210					215	
ATG	TGC	CGA	GTG	AAG	ACA	CTG	CCA	GAC	CGG	ACA	TGG	ACC	TAC	TCC	TTC	726
Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	Arg	Thr	Trp	Thr	Tyr	Ser	Phe	
				220					225					230		
TCC	GGA	GCC	TTC	CTG	TTC	TCC	ATG	GGC	TTC	CTC	GTC	GCA	GTA	CTC	TGC	774
Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	Phe	Leu	Val	Ala	Val	Leu	Cys	
			235					240					245			

TAC	CTG	AGC	TAC	AGA	TAT	GTC	ACC	AAG	CCG	CCT	GCA	CCT	CCC	AAC	TCC	822
Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	Pro	Pro	Ala	Pro	Pro	Asn	Ser	
		250					255					260				
CTG	AAC	GTC	CAG	CGA	GTC	CTG	ACT	TTC	CAG	CCG	CTG	CGC	TTC	ATC	CAG	870
Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	Gln	Pro	Leu	Arg	Phe	Ile	Gln	
	265					270					275					
GAG	CAC	GTC	CTG	ATC	CCT	GTC	TTT	GAC	CTC	AGC	GGC	CCC	AGC	AGT	CTG	918
Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	Leu	Ser	Gly	Pro	Ser	Ser	Leu	
280					285					290					295	
GCC	CAG	CCT	GTC	CAG	TAC	TCC	CAG	ATC	AGG	GTG	TCT	GGA	CCC	AGG	GAG	966
Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	Arg	Val	Ser	Gly	Pro	Arg	Glu	
				300					305					310		
CCC	GCA	GGA	GCT	CCA	CAG	CGG	CAT	AGC	CTG	TCC	GAG	ATC	ACC	TAC	TTA	1014
Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	Leu	Ser	Glu	Ile	Thr	Tyr	Leu	
			315					320					325			
GGG	CAG	CCA	GAC	ATC	TCC	ATC	CTC	CAG	CCC	TCC	AAC	GTG	CCA	CCT	CCC	1062
Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	Pro	Ser	Asn	Val	Pro	Pro	Pro	
		330					335					340				
CAG	ATC	CTC	TCC	CCA	CTG	TCC	TAT	GCC	CCA	AAC	GCT	GCC	CCT	GAG	GTC	1110
Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	Pro	Asn	Ala	Ala	Pro	Glu	Val	
	345					350					355					
GGG	CCC	CCA	TCC	TAT	GCA	CCT	CAG	GTG	ACC	CCC	GAA	GCT	CAA	TTC	CCA	1158
Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	Thr	Pro	Glu	Ala	Gln	Phe	Pro	
360					365					370					375	
TTC	TAC	GCC	CCA	CAG	GCC	ATC	TCT	AAG	GTG	CAG	CCT	TCC	TCC	TAT	GCC	1206
Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	Val	Gln	Pro	Ser	Ser	Tyr	Ala	
				380					385					390		
CCT	CAA	GCC	ACT	CCG	GAC	AGC	TGG	CCT	CCC	TCC	TAT	GGG	GTA	TGC	ATG	1254
Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	Pro	Ser	Tyr	Gly	Val	Cys	Met	
			395					400					405			
GAA	GGT	TCT	GGC	AAA	GAC	TCC	CCC	ACT	GGG	ACA	CTT	TCT	AGT	CCT	AAA	1302
Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	Gly	Thr	Leu	Ser	Ser	Pro	Lys	
		410					415					420				

CAC CTT AGG CCT AAA GGT CAG CTT CAG AAA GAG CCA CCA GCT GGA AGC	1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
425 430 435	
TGC ATG TTA GGT GGC CTT TCT CTG CAG GAG GTG ACC TCC TTG GCT ATG	1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
440 445 450 455	
GAG GAA TCC CAA GAA GCA AAA TCA TTG CAC CAG CCC CTG GGG ATT TGC	1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
460 465 470	
ACA GAC AGA ACA TCT GAC CCA AAT GTG CTA CAC AGT GGG GAG GAA GGG	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
475 480 485	
ACA CCA CAG TAC CTA AAG GGC CAG CTC CCC CTC CTC TCC TCA GTC CAG	1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln	
490 495 500	
ATC GAG GGC CAC CCC ATG TCC CTC CCT TTG CAA CCT CCT TCC GGT CCA	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
505 510 515	
TGT TCC CCC TCG GAC CAA GGT CCA AGT CCC TGG GGC CTG CTG GAG TCC	1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
520 525 530 535	
CTT GTG TGT CCC AAG GAT GAA GCC AAG AGC CCA GCC CCT GAG ACC TCA	1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser	
540 545 550	
GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC	1734
Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala	
555 560 565	
CTG ACT GTG CAG TGG GAG TCC TGAGGGGAAT GGGAAAGGCT TGGTGCTTCC TCCC	1789
Leu Thr Val Gln Trp Glu Ser	
570	
TGTCCCTACC CAGTGTACACA TCCTTGCTG TCAATCCCAT GCCTGCCCAT GCCACACACT	1849
CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAAGCAG AGGGAGTGGC ATGCAGGGCC	1909
CCTGCCATGG GTGCGCTCCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCGGGGGA	1969
GCTCTGGGGA GCAGCTTG TG TAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT	2029
GACAGTGCAA GGAGGAAATG CAGGGAAACT CCCGAGGTCC AGAGCCCCAC CTCCTAACAC	2089

CATGGATTCA	AAGTGCTCAG	GGAATTTGCC	TCTCCTTGCC	CCATTCCTGG	CCAGTTTCAC	2149
AATCTAGCTC	GACAGAGCAT	GAGGCCCTG	CCTCTTCTGT	CATTGTTCAA	AGGTGGGAAG	2209
AGAGCCTGGA	AAAGAACCAG	GCCTGGAAAA	GAACCAGAAG	GAGGCTGGGC	AGAACCAGAA	2269
CAACCTGCAC	TTCTGCCAAG	GCCAGGGCCA	GCAGGACGGC	AGGACTCTAG	GGAGGGGTGT	2329
GGCCTGCAGC	TCATTCCCAG	CCAGGGCAAC	TGCCTGACGT	TGCACGATT	CAGCTTCATT	2389
CCTCTGATAG	AACAAAGCGA	AATGCAGGTC	CACCAGGGAG	GGAGACACAC	AAGCCTTTTC	2449
TGCAGGCAGG	AGTTTCAGAC	CCTATCCTGA	GAATGGGGTT	TGAAAGGAAG	GTGAGGGCTG	2509
TGGCCCTGG	ACGGGTACAA	TAACACACTG	TACTGATGTC	ACAACTTTGC	AAGCTCTGCC	2569
TTGGGTTCAG	CCCATCTGGG	CTCAAATTCC	AGCCTCACCA	CTCACAAGCT	GTGTGACTTC	2629
AAACAAATGA	AATCAGTGCC	CAGAACCTCG	GTTTCCTCAT	CTGTAATGTG	GGGATCATAA	2689
CACCTACCTC	ATGGAGTTGT	GGTGAAGATG	AAATGAAGTC	ATGTCTTTAA	AGTGCTTAAT	2749
AGTGCCTGGT	ACATGGGCAG	TGCCCAATAA	ACGGTAGCTA	TTTAAAAAAA	AAAAAATAAT	2809
AAAAAATAAT	CGGCCGCCTC	GA				2831

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His
1				5					10					15	
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser
			20					25					30		
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr
		35					40				45				
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
	50					55				60					
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn
65					70				75					80	
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val
				85					90					95	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg
		100						105					110		
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys
		115				120						125			
Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr
	130					135					140				

Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190
 Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
 225 230 235 240
 Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
 245 250 255
 Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
 260 265 270
 Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
 275 280 285
 Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
 290 295 300
 Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
 305 310 315 320
 Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
 325 330 335
 Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
 340 345 350
 Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
 355 360 365
 Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
 370 375 380
 Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
 385 390 395 400
 Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
 405 410 415
 Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
 420 425 430
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495

Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
 565 570

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCAACTTTGA	AAACATCCTG	ACGTGGGACA	GCGGGCCAGA	GGGCACCCCA	GACACGGTCT	60
ACAGCATCGA	GTATAANACG	TACGGAGAGA	GGGACTGGGT	GGCAAAGAAN	GGCTGTCAGC	120
GGATCACCCG	GAAGTCCTGC	AACCTGACGG	TGGAGACGGG	CAACCTCACG	GAGCTCTACT	180
ATGCCAGGGT	CACCGCTGTC	AGTGCGGGAG	GCCGGTCANC	CACCAAGATG	ACTGACAGGT	240
TCAGCTCTCT	GCAGCACACT	ACCCTCAAGC	CACCTGATGT	GACCTGTATC	TCCAAAGTGA	300
GATCGATTCT	GATGATTGTT	CATCCTACCC	CCACGCCAAT	CCGTGCAGGC	GATG	354

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AACATCCTGA CGTGGGACAG CGGGCCAGAG

30

(2) INFORMATION FOR SEQ ID NO:5:

004290-EST-62260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTISENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGTCACA TCAGGTGGCT TGAGGGTAGT

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCTGGGTTC GCTACTCGAG GCGGCCGCTA TTTTTTTTTT TTTTTTTT

48

004290 EST 02E60